

Figure 1 Plasmid pCMV.Bx08.gp160

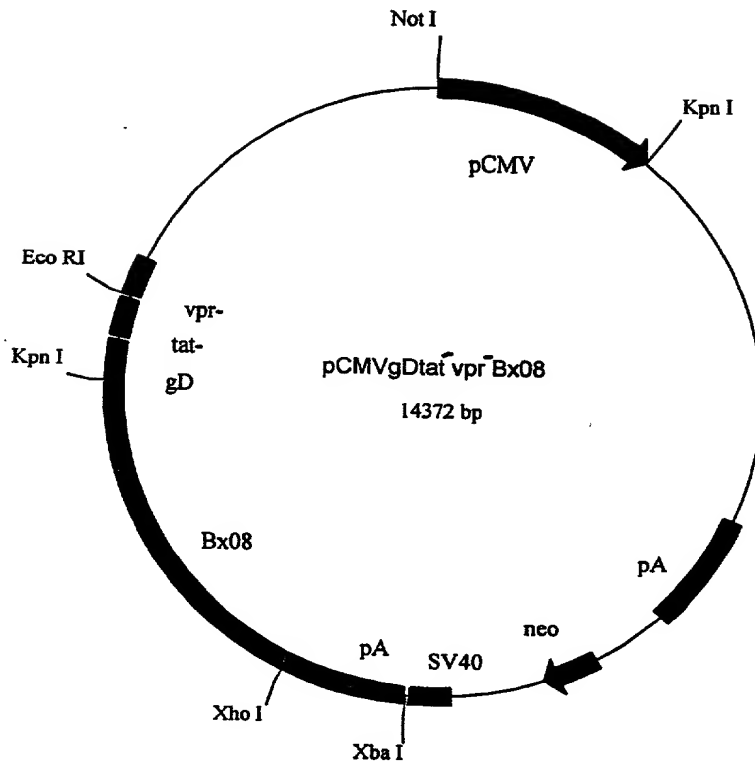


Figure 2 DNA immunization plasmid pCMV3Bx08.

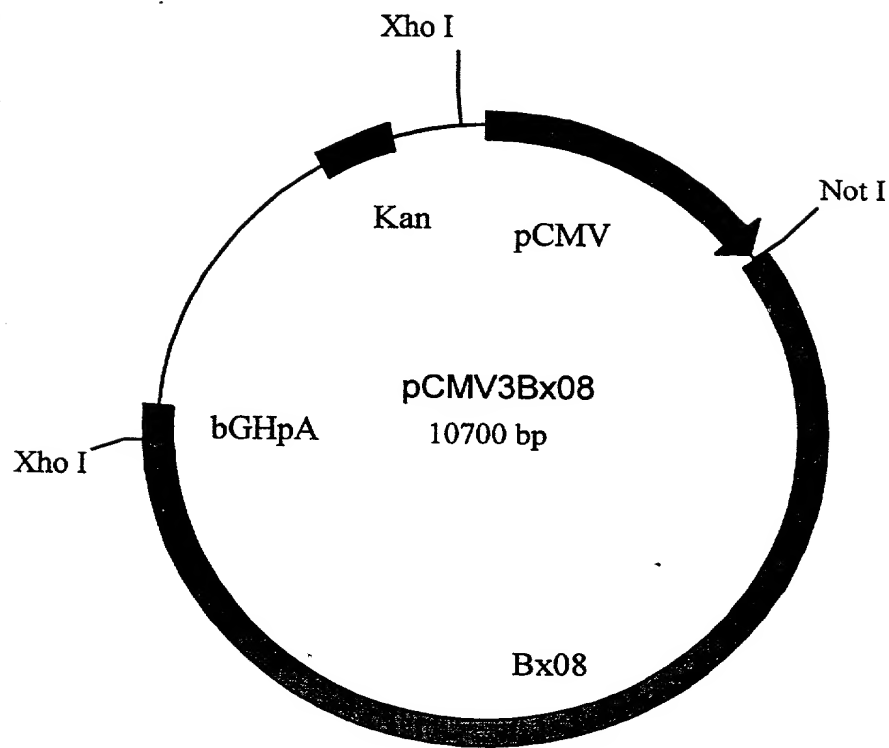
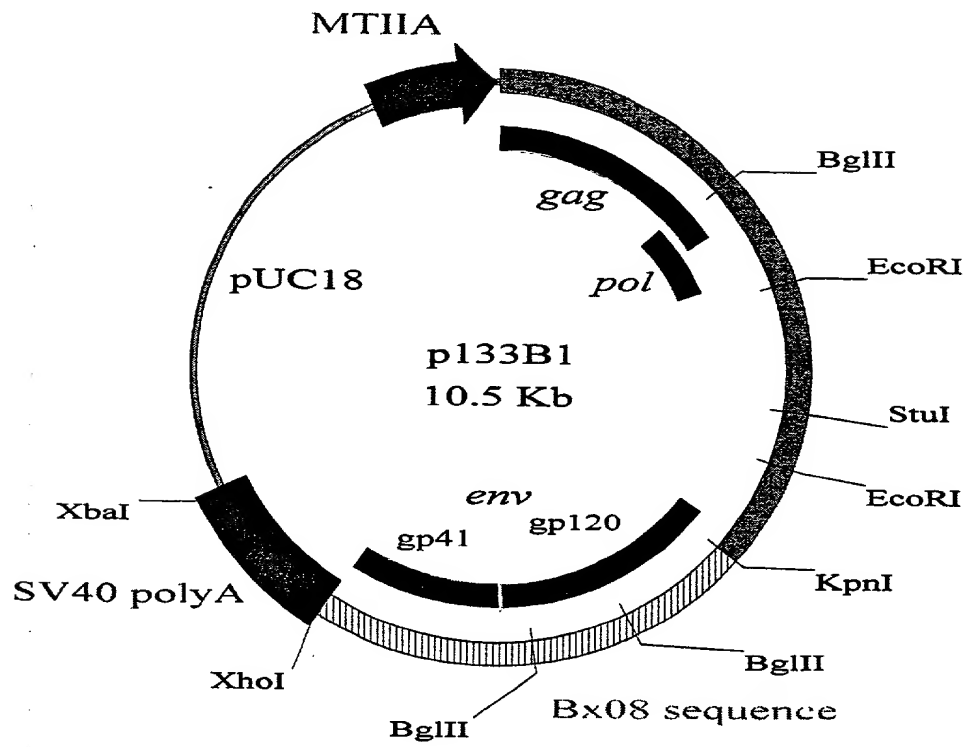


Figure 3. Pseudovirion Expression Plasmid p133B1 HIV-1 Bx08



[illegible]

**Figure 1: Time line of FMC-vaccine**

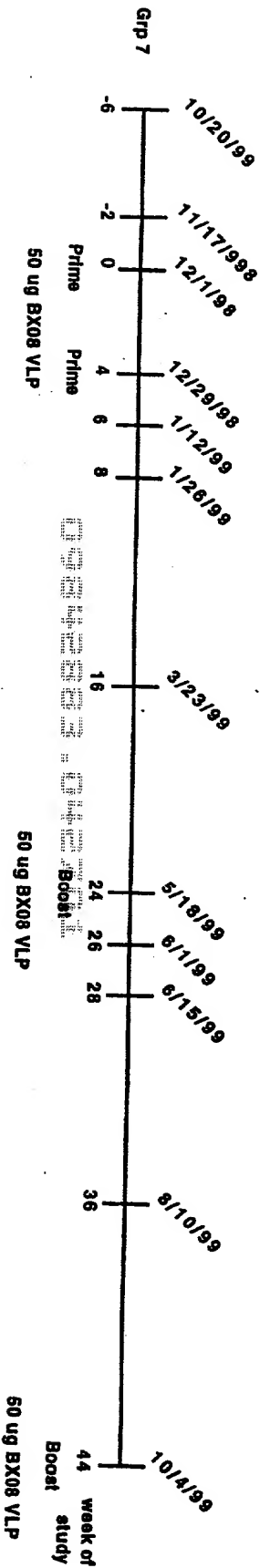
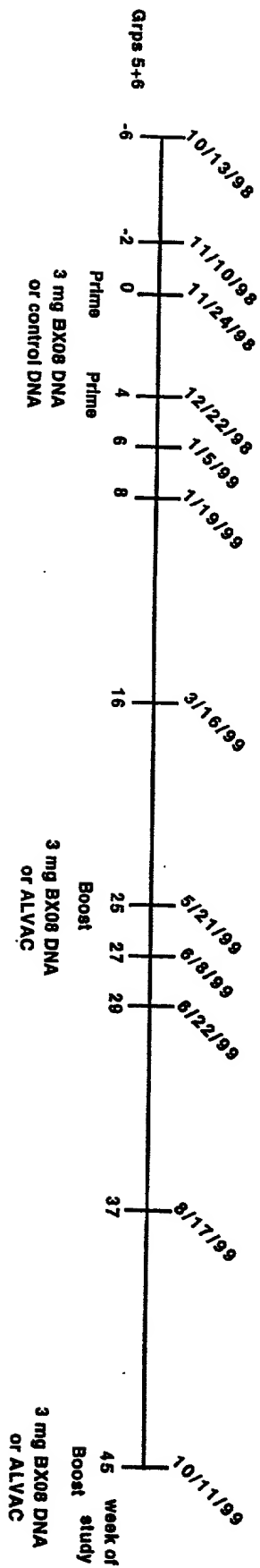
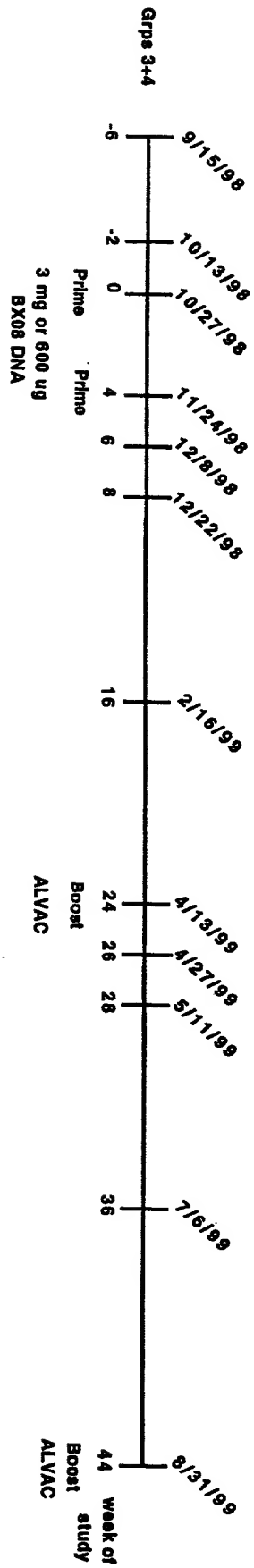
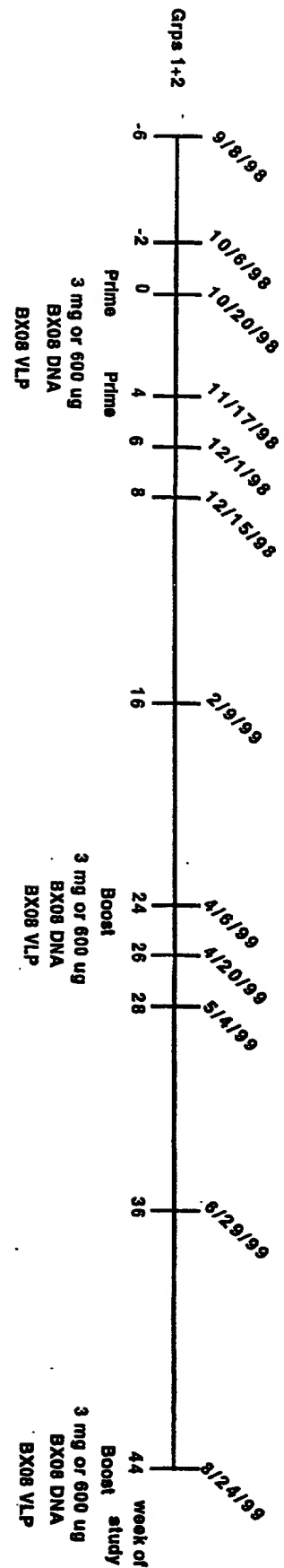
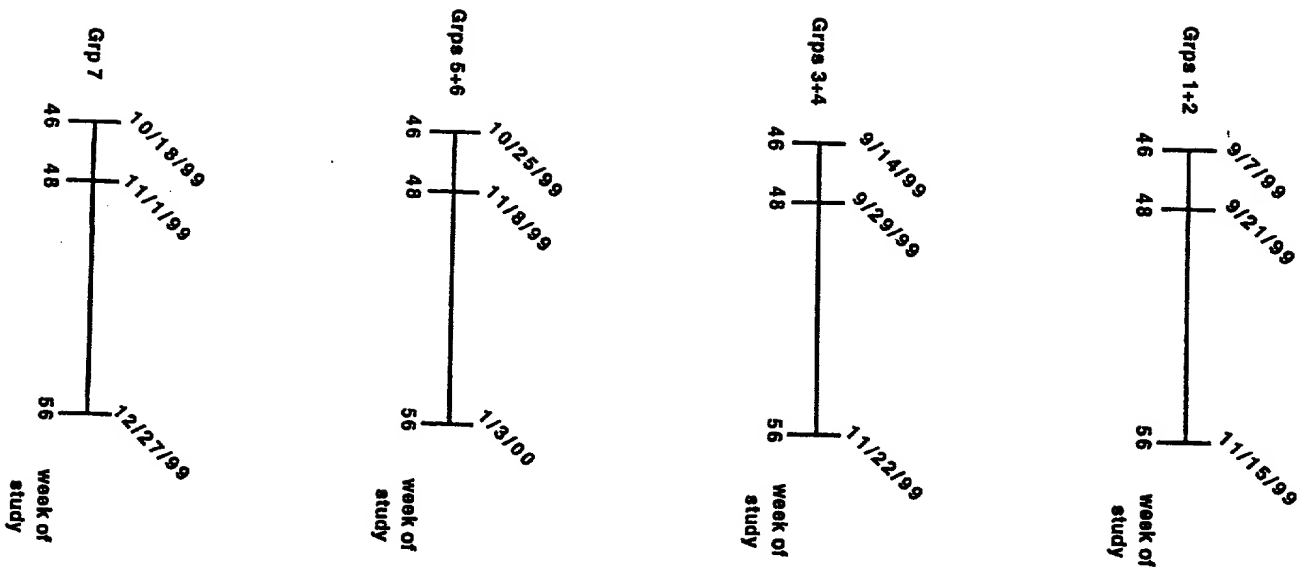
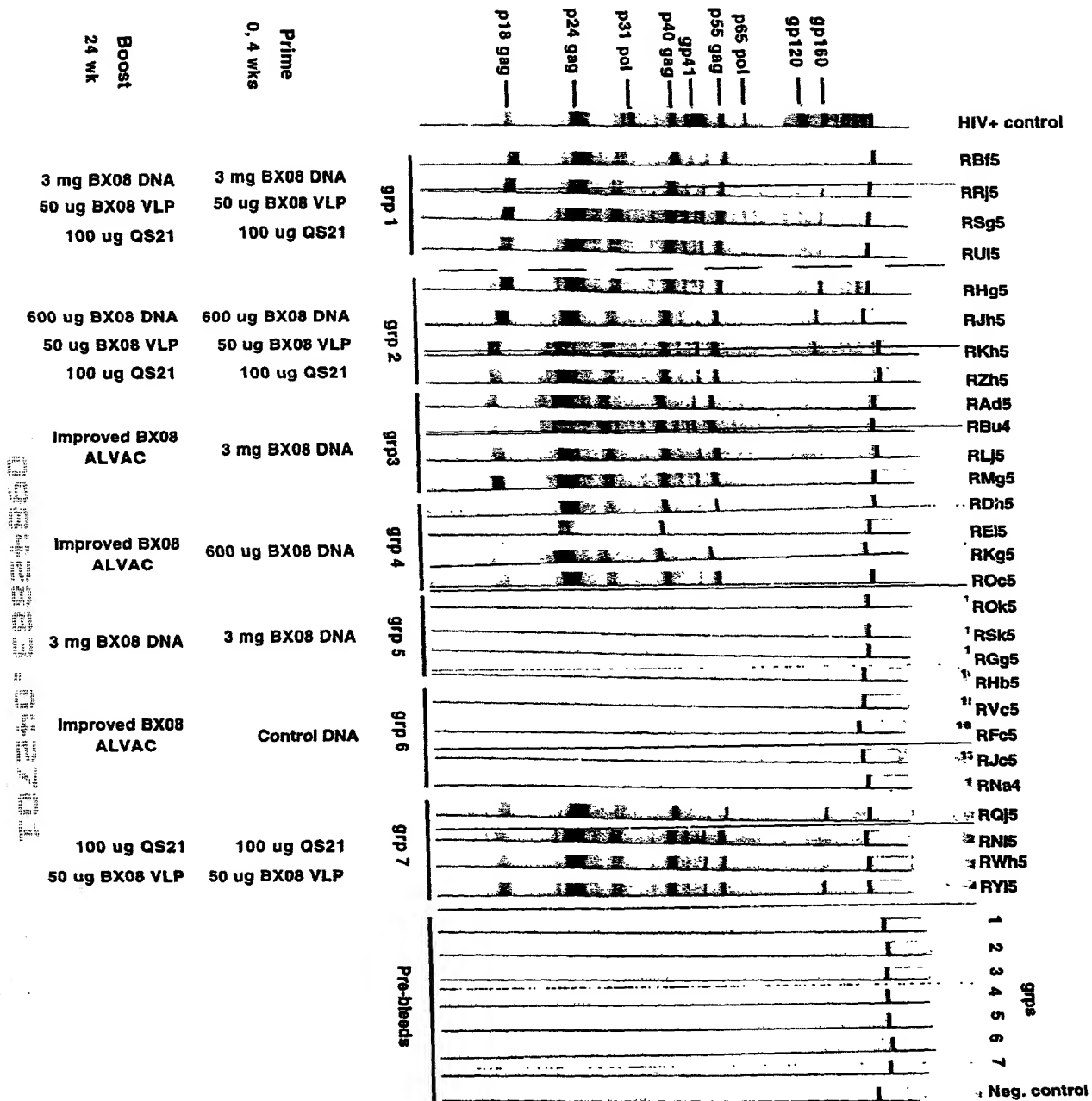


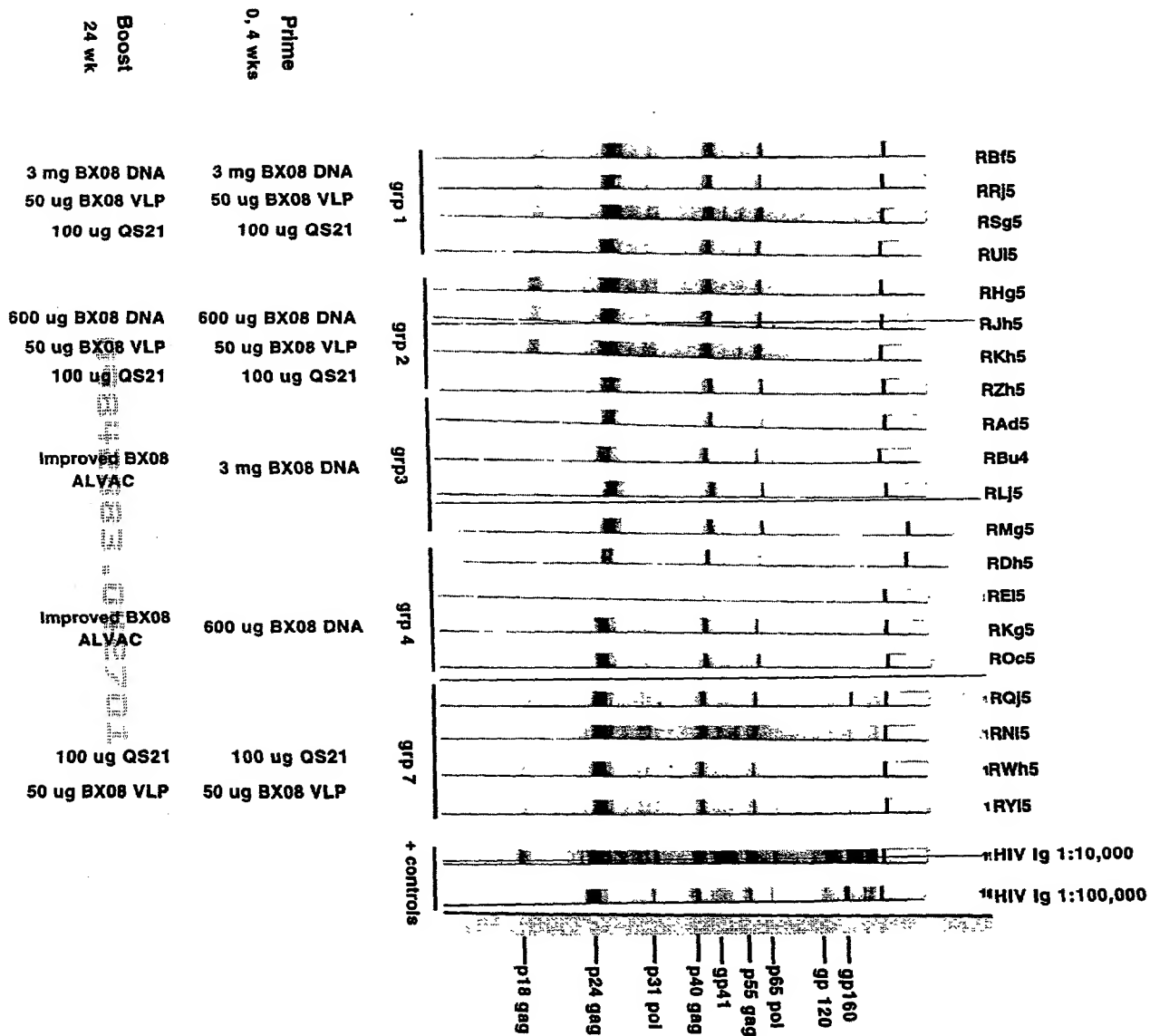
Figure 1 continued



Each study group is a group of subjects who were assigned to a specific treatment group. The subjects were then followed up over time to see how they responded to the treatment. The data from these studies are used to evaluate the effectiveness of the treatment.



647  
 Figure 3. 26 wk macaque serum immunoreactivity to HIV antigens (1:1000 diln)

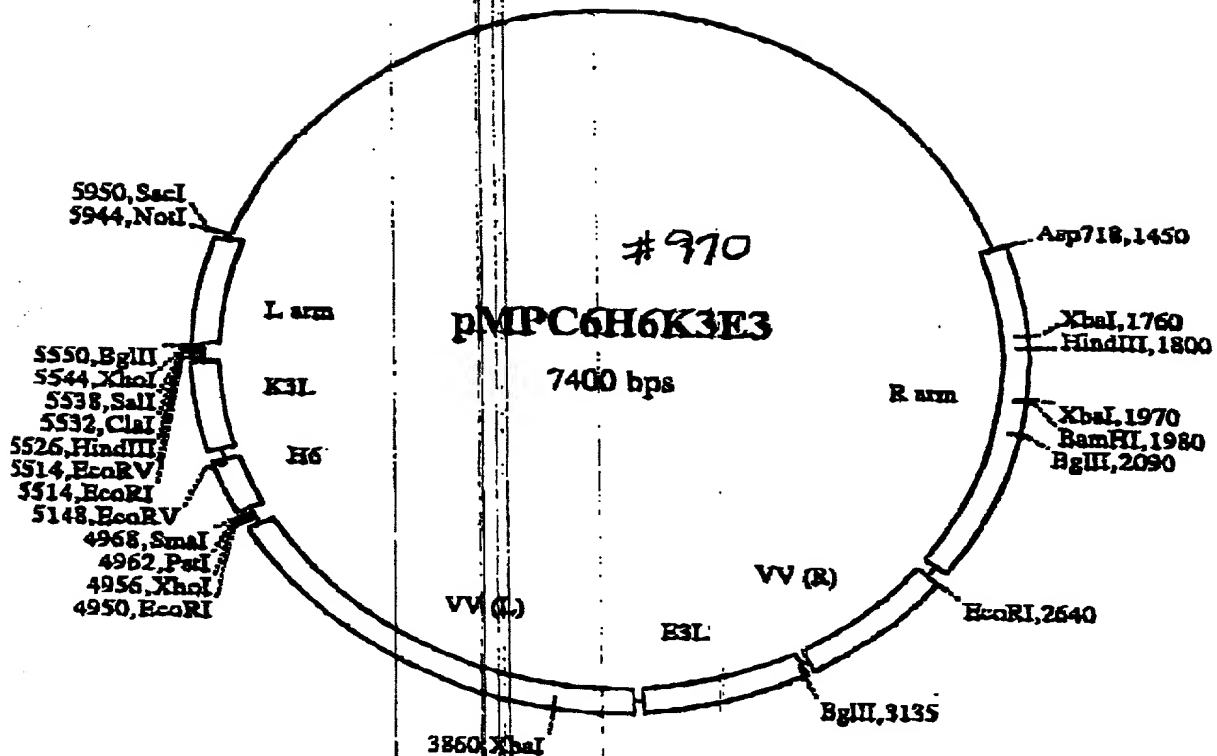




9/15

2-14-Pox.R

7.8



2-110-HIV

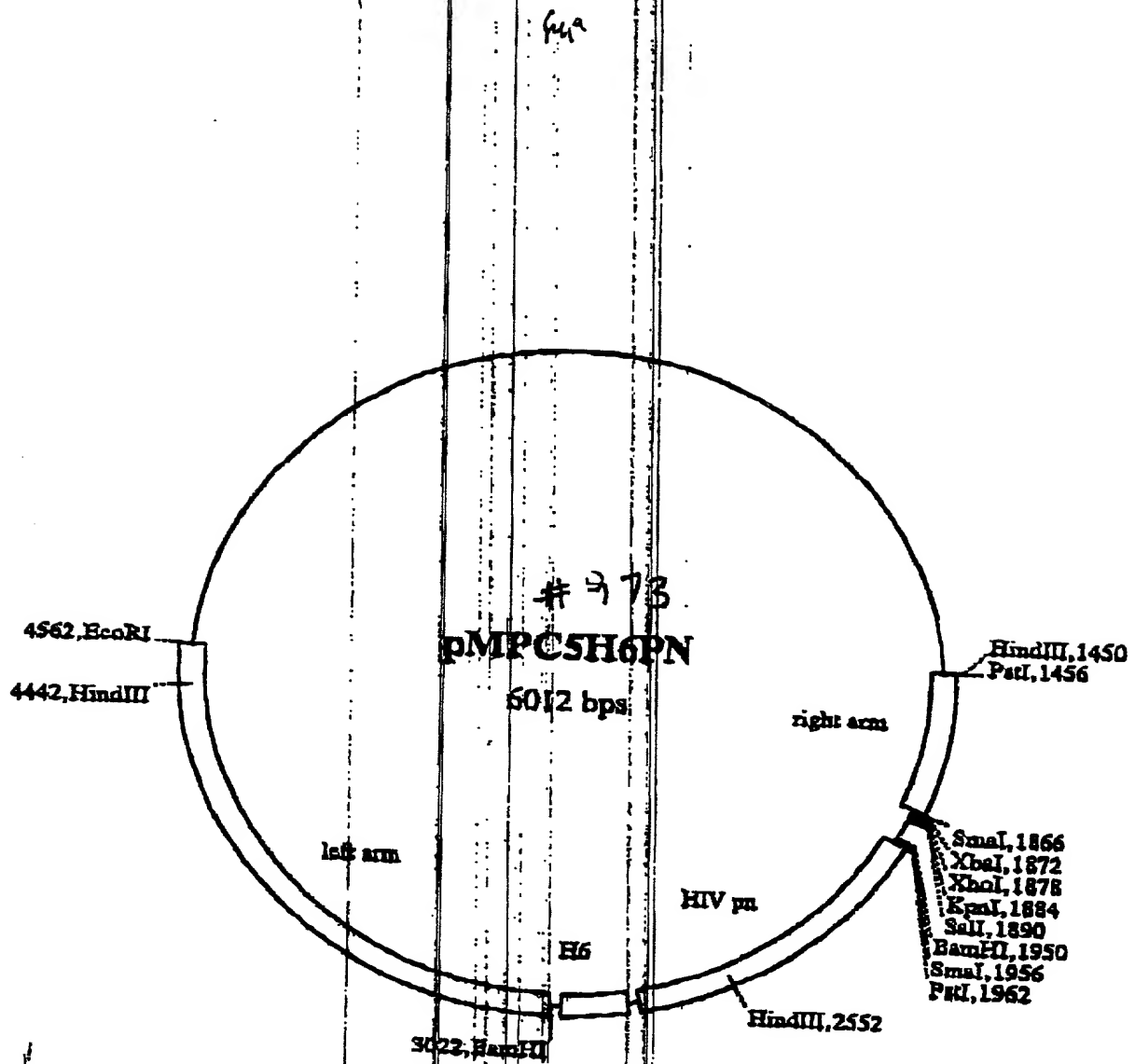


Figure 10 Plasmid pHIV76

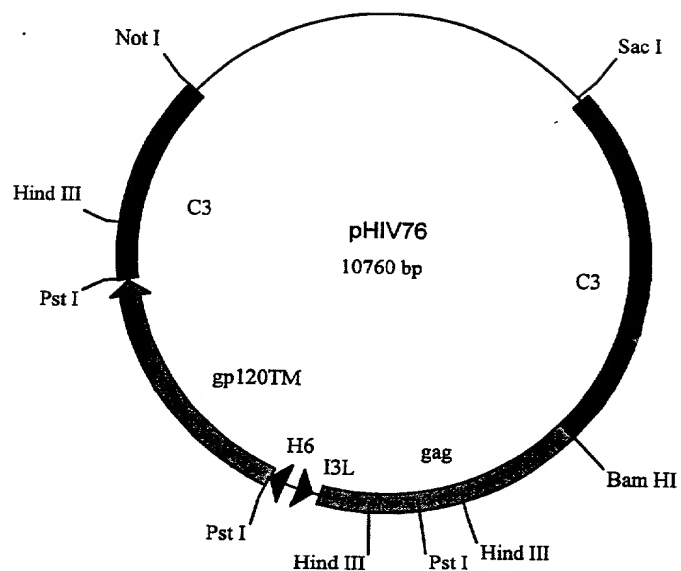


Figure 11

vCP1579: H6/HIV Pol/Nef epitope cassette in ALVAC C5 site

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  1 TTTTTCATCAT TATTTAGAAA TTATGCATTT TAGATCTTTA TAAGCGGCCG TGATTAACATA
 61 GTCATAAAAA CCCGGGATCG ATTCTAGACT CGAGGGTACC GGATCTTAAT TAATTAGTCA
121 TCAGGCAGGG CGAGAACGAG ACTATCTGCT CGTTAATTAA TTAGGTCGAC GGATCCCCCA
181 ACAAAAACTA ATCAGCTATC GGGGTTAATT AATTAGTTAT TAGACAAGGT GAAAACGAAA
241 CTATTTGTTAG CTTAATTAAT TAGAGCTTCT TTATTCTATA CTTAAAAAGT GAAAATAAAT
301 ACAAAGGTTC TTGAGGGTTG TGTAAATTG AAAGCGAGAA ATAATCATAA ATTATTTTTCAT
361 TATCGCGATA TCCGTTAAGT TTGTATCGTA ATGCCACTAA CAGAAGAAGC AGAGCTAGAA
421 CTGGCAGAAA ACAGAGAGAT TCTAAAAGAA CCAGTACATG GAGTGTATTA TGACCCATCA
481 AAAGACTTAA TAGCAGAAAT ACAGAAGCAG GGGCAAGGCC AATGGACATA TCAAATTTAT
541 CAAGAGCCAT TTAAAAATCT GAAAAACAGGA ATGGAGTGGA GATTTGATTC TAGATTAGCA
601 TTTCATCACG TAGCTAGAGA ATTACATCCT GAATATTTTA AAAATTGTAT GGCAATATTC
661 CAAAGTAGCA TGACAAAAAT CTTAGAGCCT TTTAGAAAAC AAAATCCAGA CATAGTTATC
721 TATCAATACA TGGATGATTT GTATGTAGGA TCTGACTTAG AAATAGGGCA GCATAGAACA
781 AAAATAGAGG AGCTGAGACA ACATCTGTTG AGGTGGGGAC TTACAACCAT GGTAGGTTTT
841 CCAGTAACAC CTCAAGTACC TTTAAGACCA ATGACTTACA AAGCAGCTGT AGATCTTTCT
901 CACTTTTTTAA AAGAAAAAGG AGGTTTAGAA GGGCTAATTC ATTCTCAACG AAGACAAGAT
961 ATTCTTGATT TGTGGATTTA TCATACACAA GGATATTTTC CTGATTGGCA GAATTACACA
1021 CCAGGACCAG GAGTCAGATA CCCATTAACC TTTGGTTGGT GCTACAAGCT AGTACCAATG
1081 ATTGAGACTG TACCAGTAAA ATTAAAGCCA GGAATGGATG GCCCAAAAGT TAAACAATGG
1141 CCATTGACAG AAGAAAAAAT AAAAGCATTG GTAGAAATTT GTACAGAGAT GGAAAAGGAA
1201 GGGAAAATTT CAAAAATTGG GCCTTAATTT TTCTGCAGCC CGGGGGATCC TTTTATAGC
1261 TAATTAGTCA CGTACCTTTG AGAGTACCAC TTCAGCTACC TCTTTTGTGT CTCAGAGTAA
1321 CTTTCTTTAA TCAATTCCAA AACAG

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Upstream (right) flanking sequence: 1-266

VV H6 promoter: 267-390

HIV pol/nef/pol/nef/pol cassette: 391-1227

Downstream (left) flanking sequence: 1227-1345

Figure 12

## E3L and K3L genes in C6

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      10      20      30      40      50      60      70      80      90      100      110
* * * * *
GAGCTCGCGG CCGCCTATCA AAAGTCTTAA TGAGTTAGGT GTAGATAGTA TAGATATTAC TACAAAGGTA TTCATATTTC CTATCAATTC TAAAGTAGAT GATATTAATA
CTCGAGCGCC GCGCGATAGT TTTCAGAAAT ACTCAATCCA CATCTATCAT ATCTATAATG ATGTTTCCAT AAGTATAAAG GATAGTTAAG ATTTCATCTA CTATAATTAT

      120      130      140      150      160      170      180      190      200      210      220
* * * * *
ACTCAAGAT GATGATAGTA GATAATAGAT ACGCTCATAT AATGACTGCA AATTITGGACG GTTCACATTT TAATCATCAC GCGTTCATAG GTTCAACTG CATAGATCAA
TGAGTTTCTA CTACTATCAT CTATTATCTA TCGGAGTATA TTACTGACGT TTAAACCTGC CAAAGTGAAA ATTAGTAGTG CGCAAGTATT CAAAGTTGAC GTATCTAGTT

      230      240      250      260      270      280      290      300      310      320      330
* * * * *
AATCTCACTA AAAAGATAGC CGATGTATTT GAGAGAGATT GGACATCTAA CTACGCTAAA GAAATTACAG TTATAAATAA TACATAATGG ATTTTGTAT CATCAGTTAT
TTAGAGTGAT TTTTCTATCG GCTACATAAA CTCTCTCTAA CCTGTAGATT GATGCGATTT CTTTAATGTC AATATTATT ATGTATTACC TAAACAATA GTAGTCAATA

      340      350      360      370      380      390      400      410      420      430      440
* * * * *
AATTACATA AGTACAATAA AAAGTATTAA ATAAAAATAC TTACTTACGA AAAAATGACT AATTAGCTAT AAAAACCCAG ATCTCTCGAG GTGACCGTA TCGATAGCT
TAAATGTAT TCATGTATT TTTCATAATT TATTTTATG AATGAATGCT TTTTACTGA TTAATCGATA TTTTGGGTC TAGAGAGCTC CAGCTGCCAT AGCTATTGCA

      450      460      470      480      490      500      510      520      530
* * * * *
TGATATCGAA TTCATAAAAA TT A TTG ATG TCT ACA CAT OCT TTT GTA ATT GAC ATC TAT ATA TCC TTT TGT ATA ATC AAC TCT AAT CAC TTT
ACTATAGCTT AAGTATTTTT AA T AAC TAC AGA TGT GTA GGA AAA CAT TAA CTG TAG ATA TAT AGG AAA ACA TAT TAG TTG AGA TTA GTG AAA
<Q H R C M R K Y N V D I Y G K T Y D V R I V K
-----K3L-----

      540      550      560      570      580      590      600      610      620
* * * * *
AAC TTT TAC AGT TTT CCC TAC CAG TTT ATC CCT ATA TTC AAC ATA TCT ATC CAT ATG CAT CTT AAC ACT CTC TGC CAA GAT AGC TTC AGA
CAC TCC TAT CAG TTT TTC TAT TTA CAT ATC TCG TAT TAG GAA GAG CAT ATG AGA CCG GAA ATA ATG TAG CGG GCG TAA CCC GTT GCT TAT
<V K V T K G V L K D R Y E V Y R D M H M K V S E A L I A E S
-----K3L-----

      630      640      650      660      670      680      690      700      710
* * * * *
GTG AGG ATA GTC AAA AAG ATA AAT GTA TAG AGC ATA ATC CTT CTC GTA TAC TCT GCC CTT TAT TAC ATC GCC GCG ATT GGG CAA CGA ATA
CAC TCC TAT CAG TTT TTC TAT TTA CAT ATC TCG TAT TAG GAA GAG CAT ATG AGA CCG GAA ATA ATG TAG CGG GCG TAA CCC GTT GCT TAT
<H P Y D F L Y I Y L A Y D K E Y V R G K I V D G A N P L S Y
-----K3L-----

      720      730      740      750      760      770      780      790      800      810
* * * * *
ACA AAA TGC AAG CMT ACG ATACAACTT AACGGATATC GCGAATATGA AATAATTAT GATTATTCTT CGCTTTCAAT TTAACACAAC CCTCAAGAAC
TGT TTT ACG TTC GTA TGC TATGTTTGAA TTGCTTATAG CGCTATTACT TTATTAAATA CTAATAAAGA GCGAAAGTTA AATTGTGTGG GGAGTTCTTG
<C F A L M
-----K3L-----

      820      830      840      850      860      870      880      890      900      910      920
* * * * *
CTTTGTATTT ATTTTCACTT TTAAAGTATA GAATAAAGAA AGCTCTAATT AATTAAATGAA CAGATTGTTT CGTTTTCCTT TTGGCGTATC ACTAATTAAAT TAACCCGGGC
GAAACATAAA TAAAGTGAA AAATTCATAT CTTATTCTT TCGAGATTAA TTAATTACTT GTCTAACAAA GCAAAAGGGG AACCAGCATG TGATTAATTA ATTGGCCCGC

      930      940      950      960      970      980      990      1000      1010      1020      1030
* * * * *
TGCAGCTCGA GGAATTCAAC TATATCGACA TATTTCAATT GTATACACAT AACCATTTACT AACGTAGAAT GTATAGGAAG AGATGTAACG GGAACAGGGT TTGTTGATTC
ACGTGCGCT CCTTAAGTTG ATATAGCTGT ATAAAGTAAA CATATGTGTA TTGGTAATGA TTGCATCTTA CATATCTTTC TCTACATTGC CCTTGTCCCA AACAACTAAG

      1040      1050      1060      1070      1080      1090      1100      1110      1120      1130      1140
* * * * *
GCAAACTATT CTAATACATA ATTCITCTGT TAATACGTCT TGCAGGTAAT CTATTATAGA TGCCAAGATA TCTATATAAT TATTTGTAA GATGATGITA ACTATGTGAT
CGTTTGATAA GATTATGTAT TAAGAAGACA ATTATGCAGA ACGTGCAATTA GATAATATCT ACGGTTCTAT AGATATATTA ATAAACACT CTACTACAAAT TGATACACTA

      1150      1160      1170      1180      1190      1200      1210      1220      1230      1240      1250
* * * * *
CTATATAAGT AGTGAATAAA TTCAATGTAAT TCGATATATG TTCCAACCTCT GTCTTTTGTA TGTCTAGTTT CGTAATATCT ATAGCATCTC CAAAAATAT ATTGCGATAT
GATATATTCA TCACATATT AAGTACATAA AGCTATATAC AAGGTGAGA CAGAAACACT ACAGATCAAA GCATTATAGA TATCGTAGGA GTTTTATTATA TAAGCGTATA

      1260      1270      1280      1290      1300      1310      1320      1330      1340      1350      1360
* * * * *
ATTCCCAAGT CTTCACTTCT ATCTCTCTAA AAATCTTCAA CGTATGGAAT ATAATAATCT ATTTTACCTC TTCTGATATC ATTAATGATA TAGTTTTTGA CACTATCTTC
TAAGGGTTCA GAAGTCAAGA TAGAAGATT TTTAGAAGTT GCATACCTTA TATTATTAGA TAAATGGAG AAGACTATAG TAATTACTAT ATCAAAACT GTGATAGAAG

      1370      1380      1390      1400      1410      1420      1430      1440      1450      1460      1470
* * * * *
TGTCATTTGA TTCTATTCA CTATATCTAA GAAACGATA GCGTCCCTAG GACGAACCTAC TGCCATTAAT ATCTCTATTA TAGCTTCTGG ACATAATTCA TCTATTATAC
ACAGTTAACT AAGAATAAGT GATATAGATT CTTTGCTTAT CCGAGGATC CTGCTTGATG ACGGTAATTA TAGAGATAAT ATCGAAGACC TGTATTAGT AGATAATATG

      1480      1490      1500      1510      1520      1530      1540      1550      1560      1570      1580
* * * * *
CAGAAATTAAT GGGAACTATT CCGTATCTAT CTAACATAGT TTTAAGAAAG TCAGAATCTA AGACCTGATG TTCATATATT GGTTCATACA TGAATGATC TCTATTGATG
GCTTAATTA CCCTTGATAA GGCATAGATA GATTGTATCA AAATTCCTTC AGCTTAGAT TCTGGACTAC AAGTATATAA CCAAGTATGT ACTTTACTAG AGATAACTAC

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TATCACTGAT AAAGTAAGAG ACTTTTAACC ATTGAGTAAG ATATATACGA AAGGAACAAC TACTTCTAT CTTATATGAG TTATCTTAAA CATGTTGTGT TGACAAGAGA

1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800  
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ATACTTAGCA TATAGTAGTA GACTTTATTA GTACATTCGG TATGTAAATT GTTAATCTCT GAACAGAGGA CAATAGTTAT ATGATAAGAA CACTATTAAA TACACACTCC

1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910  
CAAAATTTGTC CACGTTCTTT AATTTTGTTA TAGTAGATAT CAAATCCAAT GGAGCTACAG TTCTTGGCTT AAACAGATAT AGTTTTTCTG GAACAAATTC TACAACATTA  
GTTTAAACAG GTGCAAGAAA TTAAACAAT ATCATCTATA GTTTAGGTTA CCTCGATGTC AAGAACCAGAA TTGTCTATA TCARAAAGAC CTGTTTAAAG ATGTTGTAAT

1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020  
TTATAAGGA CTTTGGGTAG ATAAAGTGGG TGAATCCTA TTTTAATPAA TGCTATCGCA TTGTCTCTCT GCAATATATCC AAACGCTTTT GTGATAGTAT GGCATTCAAT  
AATATTTCCT GAAACCCATC TATTCACCTT ACTTTAGGAT AAAATTAATT ACGATAGCGT AACAGGAGCA CGTTTATAGG TTTGCGAAAA CACTATCATA CGTAAGTAA

2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130  
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CAGATCTTTG CGAGATGCTT ATAGACACTG TCTATAGTAG AAATCTCTTA TATGATCAGC GCAATTATCA TGATGTTAAA CATAAAAAT TAGATAGAGT TATTTTTTA

2140 2150 2160 2170 2180 2190 2200 2210 2220 2230  
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ATTATACATA CTAAGTTACA TATTGATTG ATGATTGACA ATAATAATT ATCTTAGT CTT AGA TTA CTA CTG CAT TGG TTC TTC AAA TAG ATG ACG GTT  
<F R I I V Y G L L K D V A L  
-----E3L-----

2240 2250 2260 2270 2280 2290 2300 2310 2320  
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AAA TCG ACG TAA TAA AAA TCG TAG AGC AAA TCT AAA AGG TAG ACG GAA TAG CTT ATG AGA AGG CAG CTA CAG ATG TGT CCG TAT TTT ACA  
<K A A N N K A D R K S K G D A K D F V R G D I D V C A Y F T  
-----E3L-----

2330 2340 2350 2360 2370 2380 2390 2400 2410  
AGG AGA GAT ACT AGG CCC AAC TGA TTC AAT ACG AAA AGA CCA ATC TCT TCT TAG AGA GAA TCA ATA AAC CGT CAT GAG TAA TTA CCA CTG TCC CAA  
TCC TCT CAA TGA TCC GGG TTG ACT AAG TTA TGC TTT TCT GGT TAG AGA GAA TCA ATA AAC CGT CAT GAG TAA TTA CCA CTG TCC CAA  
<P S N S P G V S E I R F S W D R K T I Q C Y E N I I T V P N  
-----E3L-----

2420 2430 2440 2450 2460 2470 2480 2490 2500  
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TCG TAG AAA GGT TAG TTA TTA AAA AAA TCG GCC TTA TTG TAG TAG TTT TCT GAA TAC TAG GAG AGA GTA ACT AAA AAG CGC CCT ATG TAG  
<A D K W D I I K X A P I V D D F S K H D E R M S K E S V D  
-----E3L-----

2510 2520 2530 2540 2550 2560 2570 2580 2590  
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TAG ATA ATA CTG CAG TCG GTA TCG TAG TCG TAG GCC GAA TAG GCG GAG GCA ACA GTA TTT GGT TGC TCC TCC TTA TAG CAG CTT CGA CAT  
<D I I V D A M A D A D P K D A E T T M F W R P P I D D S S Y  
-----E3L-----

2600 2610 2620 2630 2640 2650 2660 2670 2680  
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<V M A S R Q L D Y L A K N V E R K E M N L Q R T L Q A A T A  
-----E3L-----

2690 2700 2710 2720 2730 2740 2750 2760 2770  
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<G E I G I N K I A A C V I E A D S R E D I Y I K S M  
-----E3L-----

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GATTGTGTTG GTGTTTATTT TGACTTGGAT GAAATAGTAA AAAAATAAGT AGTAGAGAC CACCAAGCAG CAAAGATAGC TTACATCGAG ACTAATTGGG CAGTAGATAT

2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990  
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CCACTACGAC CAAGACCTCT AAGACCTCTT CTACCTAATA ATAGACCTTC TGAGAGACAA TAAAGGAACA AAAGTACATA GCTAACGCAA CATTGTAAAT CTAAAGCTTT

3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100  
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ACGAGATTTA AACCTCCGA ATTTCAAC AAACGTTAGA GATGTGCGCA CAGATTGATC ACCTCCAAGC AGTCGACGAG ATCAAACTTA GTAGTAGCCG CATCATAAAG

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      *      *      *      *      *      *      *      *      *      *      *
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ATGAAAATGT CAATCCTGTG CCACATAACA TAAAGAGCAG CTCCTGCAAT TTTATTAGCA ACATTGAGTG TAGGAAATAA AATAGATATA ACATAGATGT AGGAAAGAAT

      3220      3230      3240      3250      3260      3270      3280      3290      3300      3310      3320
      *      *      *      *      *      *      *      *      *      *      *
ATGCATTTTA TACCGAATAA GAGATAGCGA AGGAATTCCT TTTATTGATT AACTAGTCAA ATGAGTATAT ATAATTGAAA AAGTAAAAAT TAAATCATAT AATAATGAAA
TACGTAAAAA ATGGCTTATT CTCTATCGCT TCCTTAAGAA AAATAACTAA TTGATCAGTT TACTCATATA TATTAACTTT TTCATTTTAT ATTTAGTATA TTATTACTTT

      3330      3340      3350      3360      3370      3380      3390      3400      3410      3420      3430
      *      *      *      *      *      *      *      *      *      *      *
CGAAATATCA GTAATAGACA GGAAC TGCCA GATTCCTCTT CTAATGAAGT AAGTACTGCT AAATCTCCAA AATTAGATAA AAATGATACA GCAAAATACAG CTTCAATCAA
GCTTTATAGT CATTATCGT CTCTGACCGT CTAAGAAGAA GATTACTTCA TTCATGACGA TTGAGAGGTT TTAATCTATT TTACTATGT CGTTTATGTC GAAGTAAGTT

      3440      3450      3460      3470      3480      3490      3500      3510      3520      3530      3540
      *      *      *      *      *      *      *      *      *      *      *
CGAATTACCT TTTAATTTT TCAGACACAC CTTATTACAA ACTAACTAAG TCAGATGATG AGAAAGTAAA TATAAATTTA ACTTATGGGT ATAATATAAT AAAGATTCAAT
GCTTAATGGA AAATTAAGAA AGTCTGTGTG GAATAATGTT TGATTGATTG AGCTACTACT TCCTTCATTT ATATTTAAT TGAATACCCA TATTATATTA TTCTAAGTA

      3550      3560      3570      3580      3590      3600      3610      3620      3630      3640      3650
      *      *      *      *      *      *      *      *      *      *      *
GATATTAAAT ATTTACTTAA CGATGTTAAT AGACTTATTC CATCAACCCC TTCAAACCTT TCTGGATATT ATAAAAATACC AGTTAATGAT AITAAAAATG ATGTGTTAAT
CTATAATTAT TAAATGAATT GCTACAATTA TCTGAATAAG GTAGTTGGGG AAGTTTGGAA AGACCTATAA TATTTTATGG TCAATTACTA TAATTTTATC TAACAAATTC

      3660      3670      3680      3690      3700      3710      3720      3730      3740      3750      3760
      *      *      *      *      *      *      *      *      *      *      *
AGATGTAAGT AATTATTGG AGTAAGAGA TATAAAATTA GTCTATCTTT CACATGGAAA TGAATTACCT AATATTAAAT ATTATGATAG GAATTTTITA GGATTATACG
TCTACATTTA TTAATTAACC TCCATTTCCT ATATTTTAAT CAGATAGAAA GTGTACCTTT ACTTAATGGA TTATAATTAT TAATACTATC CTTAAAAAAT CCTAAATGTC

      3770      3780      3790      3800      3810      3820      3830      3840      3850      3860      3870
      *      *      *      *      *      *      *      *      *      *      *
CTGTATATG TATCAACAAT ACAGGCAGAT CTATGGTAT GGTAAACAC TGTAACGGGA AGCAGCATTC TATGGTAACT GGCTATGTT TAATAGCCAG ATCATTTTAC
GACAATATAC ATAGTTGTTA TGTCCTCTA GATACCAATA CCATTTTGTG ACATTGCCCT TCGTCGTAAG ATACCATTGA CCGGATACAA ATTATCGGTC TAGTAAATG

      3880      3890      3900      3910      3920      3930      3940      3950      3960      3970      3980
      *      *      *      *      *      *      *      *      *      *      *
TCTATAAACA TTTTACCACA AATAATAGGA TCCTCTAGAT ATTTAATAT ATATCTAACA ACAACAAAAA AATTTAACGA TGTATGGCCA GAAGTATTTT CTACTAATAA
AGATAITTTT AAAATGGTGT TTATTATCCT AGGAGATCTA TAAATTATAA TATAGATTGT TGTGTGTTTT TTAATTGCT ACATACCGGT CTTCAATAAA GATGATTATT

      3990      4000      4010      4020      4030      4040      4050      4060      4070      4080      4090
      *      *      *      *      *      *      *      *      *      *      *
AGATAAGAT AGTCTATCTT ATCTACAAGA TATGAAAGAA GATAATCATT TAGTAGTAGC TACTAATATG GAAAGAAATG TATACAAAAA CGTGGAGGCT TTTTATTATA
TCTATTCTTA TCAGATAGAA TAGATGTTCT ATACTTTCTT CTATTAGTAA ATCATCATCG ATGATTATAC CTTTCTTTAC ATATGTTTTT GCACCTTCGA AATATAATT

      4100      4110      4120      4130      4140      4150      4160      4170      4180      4190      4200
      *      *      *      *      *      *      *      *      *      *      *
ATAGCATATT ACTAGAAGAT TTAATACTTA GACTTAGTAT AACAAAACAG TTAATGGCCA ATATGATTC TATATTTTCA TATAACAGTA GTACATTAAT CAGTGATATA
TATCGTATAA TGATCTTCTA AATTTTAGAT CTGAATCATA TTGTTTTGTC AATTTACGGT TATAGCTAAG ATATAAAGTA GTATTGTCA CATGTAATTA GTCATATAT

      4210      4220      4230      4240      4250      4260      4270      4280      4290      4300      4310
      *      *      *      *      *      *      *      *      *      *      *
CTGAAACGAT CTACAGACTC AACTATGCAA GGAATAAGCA ATATGCCAAT TATGTCATAT ATTTTAACCT TAGAACTAAA ACCTTCTACC AATACTAAAA ATAGGATACG
GACTTTGCTA GATGTCTGAG TTGATACGTT CCTTATTCTG TATACGGTTA ATACAGATTA TAAATTGAA ATCTTGATTT TGCAAGATGG TTATGATTTT TATCCTATGC

      4320      4330      4340      4350      4360      4370      4380      4390      4400      4410      4420
      *      *      *      *      *      *      *      *      *      *      *
TGATAGGCTG TTAAGAGCTG CAATAAATAG TAAGGATGTA GAAGAAATAC TTTGTTCTAT ACCTTGCGAG GAAAGAACTT TAGAACAACT TAAGTTTAAT CAAACTTGTA
ACTATCCGAC AATTTTGCAC GTTATTATAT ATCTCTACAT CTTCTTTATG AAACAAGATA TGGAGGCTC CTTTCTTGAA ATCTTGTTGA ATTCAAATTA GTTTGAACAT

      4430
      *      *
TTTATGAAGG TACC
AAATACTTCC ATGG

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